

Report

	assembly
# contigs (>= 1000 bp)	3
# contigs (>= 5000 bp)	2
# contigs (>= 10000 bp)	2
# contigs (>= 25000 bp)	2
# contigs (>= 50000 bp)	2
Total length (>= 1000 bp)	4226409
Total length (>= 5000 bp)	4224658
Total length (>= 10000 bp)	4224658
Total length (>= 25000 bp)	4224658
Total length (>= 50000 bp)	4224658
# contigs	4
Largest contig	4031312
Total length	4226974
Reference length	4045677
GC (%)	44.08
Reference GC (%)	43.94
N50	4031312
NG50	4031312
N75	4031312
NG75	4031312
L50	1
LG50	1
L75	1
LG75	1
# misassemblies	2
# misassembled contigs	1
Misassembled contigs length	4031312
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# unaligned contigs	0 + 2 part
Unaligned length	195013
Genome fraction (%)	99.629
Duplication ratio	1.000
# N's per 100 kbp	0.00
# mismatches per 100 kbp	1.44
# indels per 100 kbp	47.19
Largest alignment	2784820
Total aligned length	4031961
NA50	2784820
NGA50	2784820
NA75	808990
NGA75	808990
LA50	1
LGA50	1
LA75	2
LGA75	2

All statistics are based on contigs of size >= 500 bp, unless otherwise noted (e.g., "# contigs (>= 0 bp)" and "Total length (>= 0 bp)" include all contigs).

## Misassemblies report

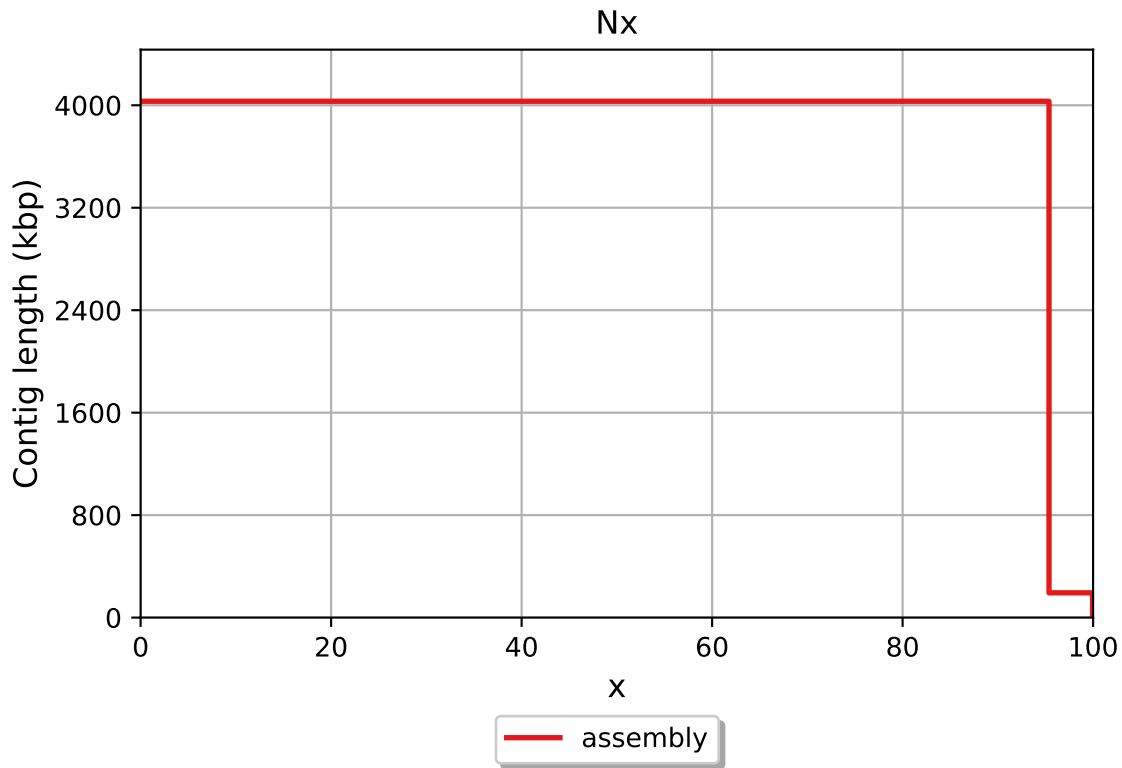
	assembly
# misassemblies	2
# contig misassemblies	2
# c. relocations	2
# c. translocations	0
# c. inversions	0
# scaffold misassemblies	0
# s. relocations	0
# s. translocations	0
# s. inversions	0
# misassembled contigs	1
Misassembled contigs length	4031312
# possibly misassembled contigs	0
# possible misassemblies	0
# local misassemblies	1
# scaffold gap ext. mis.	0
# scaffold gap loc. mis.	0
# unaligned mis. contigs	1
# mismatches	58
# indels	1902
# indels (<= 5 bp)	1897
# indels (> 5 bp)	5
Indels length	2034

All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).

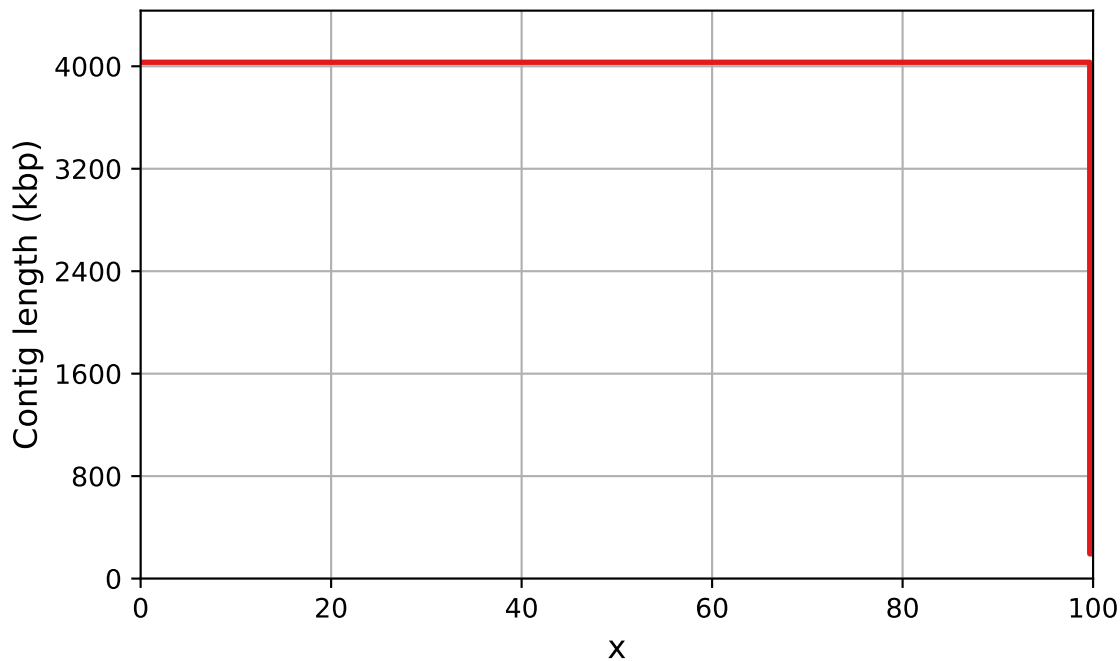
## Unaligned report

	assembly
# fully unaligned contigs	0
Fully unaligned length	0
# partially unaligned contigs	2
Partially unaligned length	195013
# N's	0

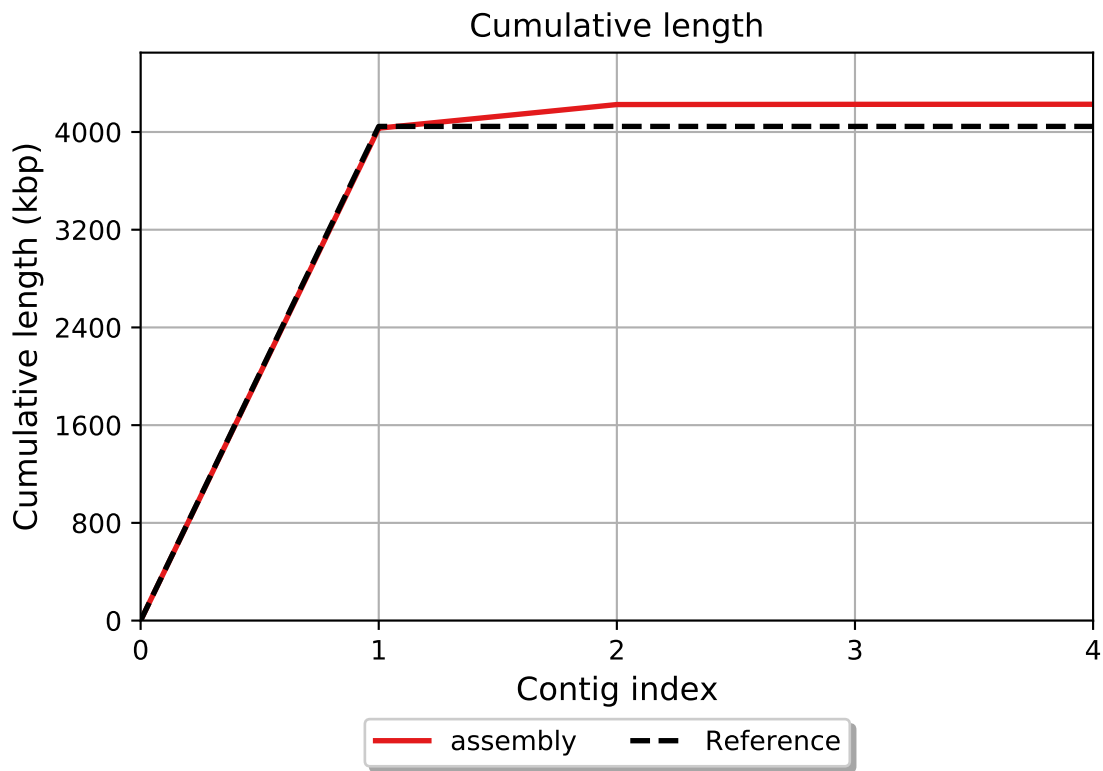
All statistics are based on contigs of size  $\geq 500$  bp, unless otherwise noted (e.g., "# contigs ( $\geq 0$  bp)" and "Total length ( $\geq 0$  bp)" include all contigs).



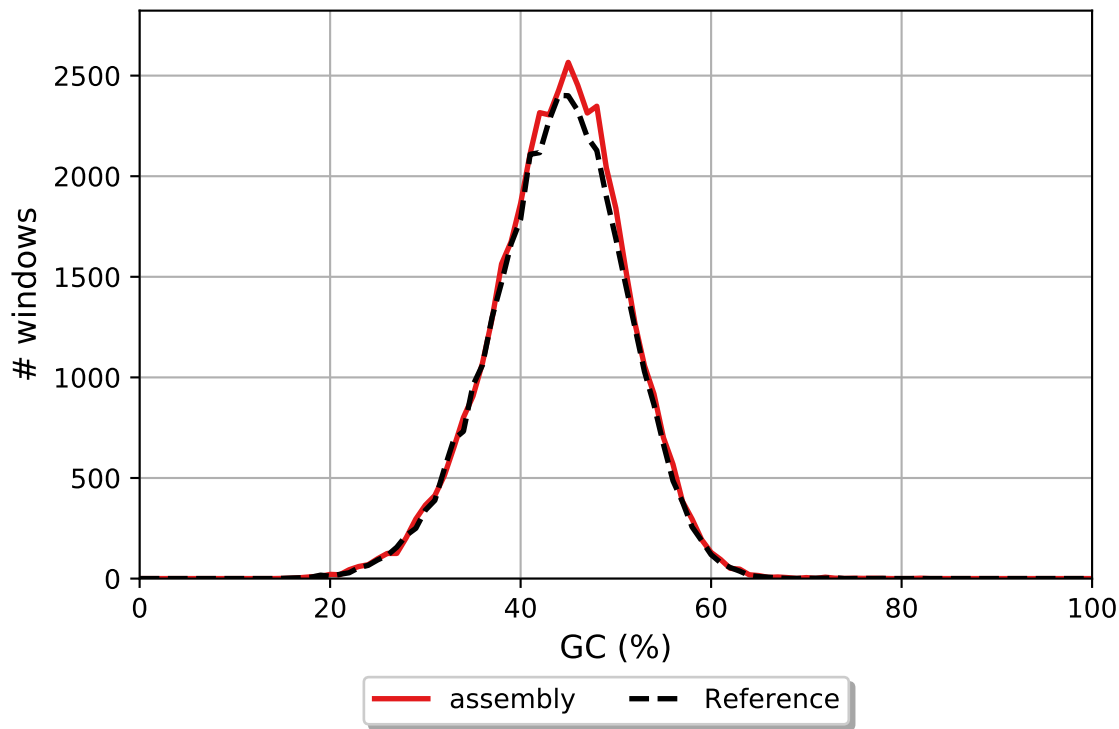
NGx



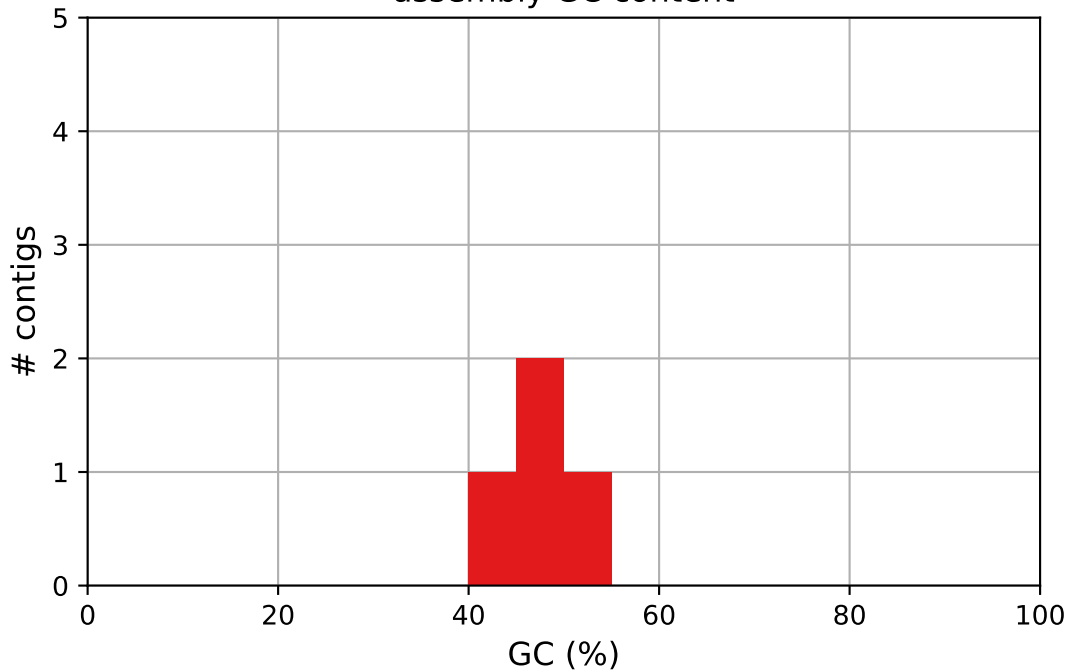
— assembly



## GC content



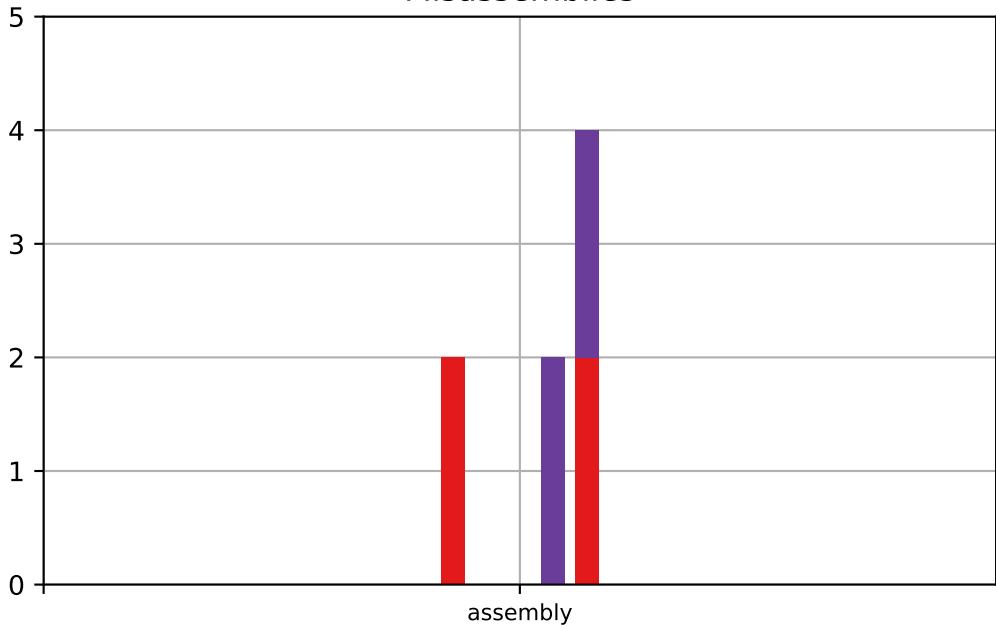
assembly GC content



assembly



## Misassemblies

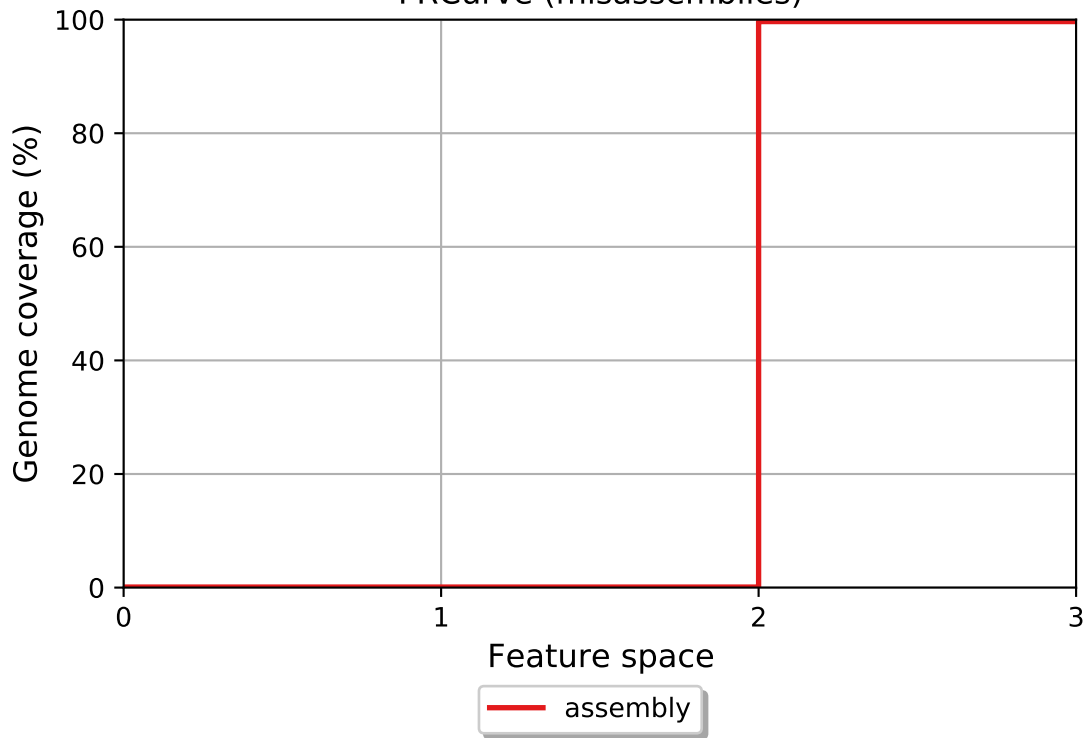


# relocations

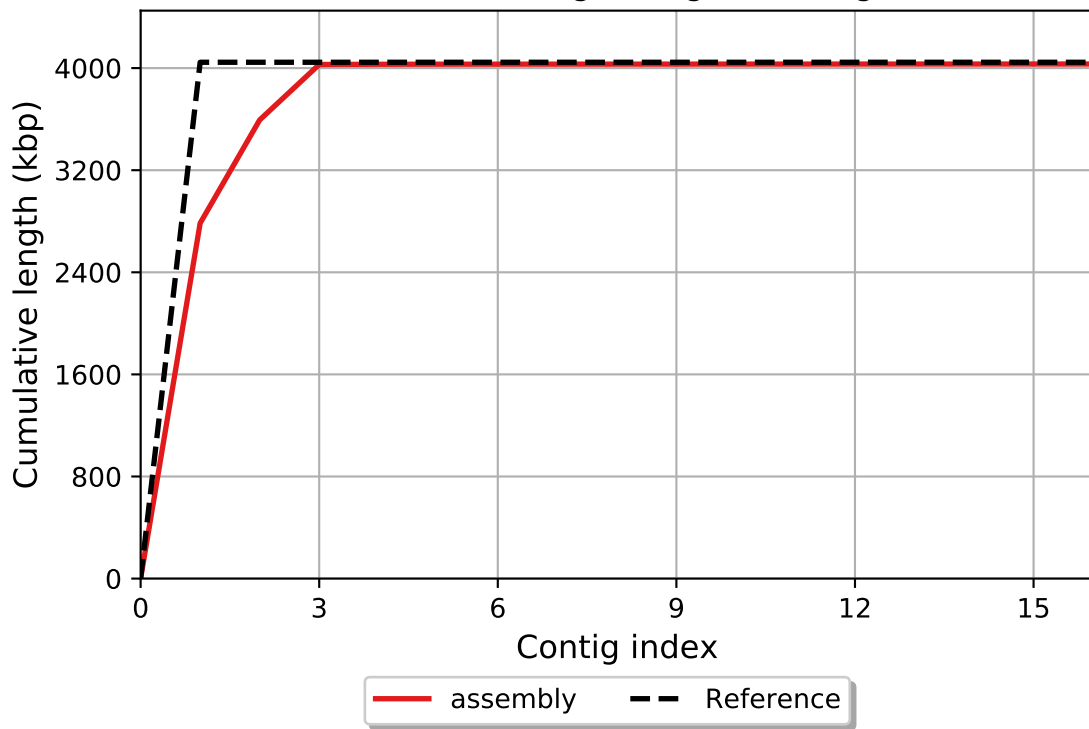


# interspecies translocations

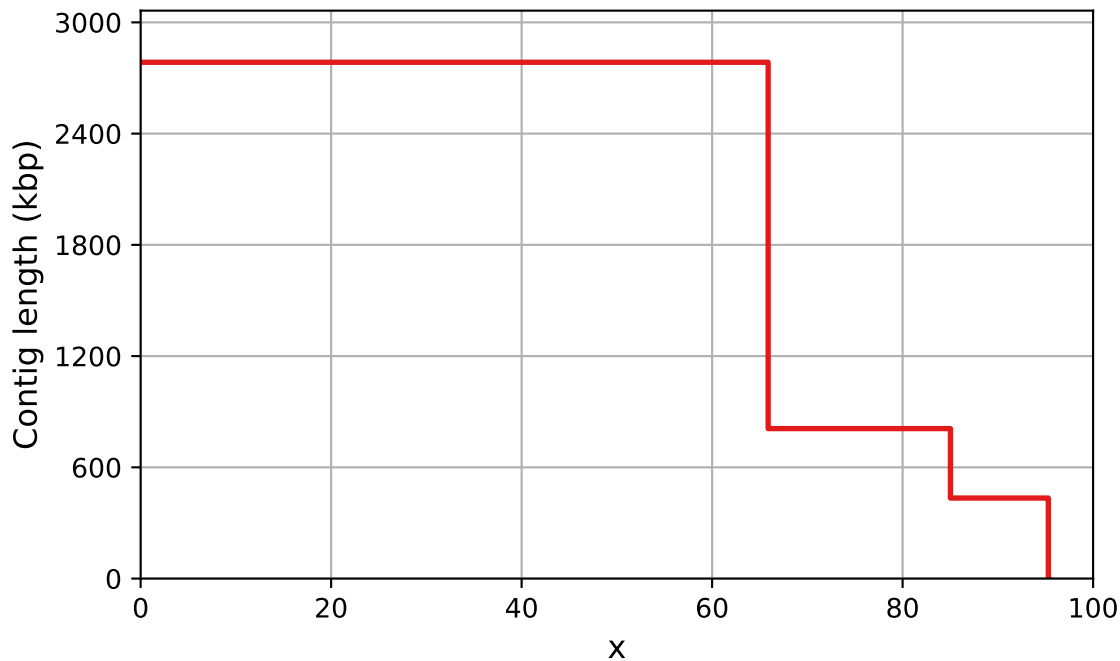
FRCurve (misassemblies)



Cumulative length (aligned contigs)

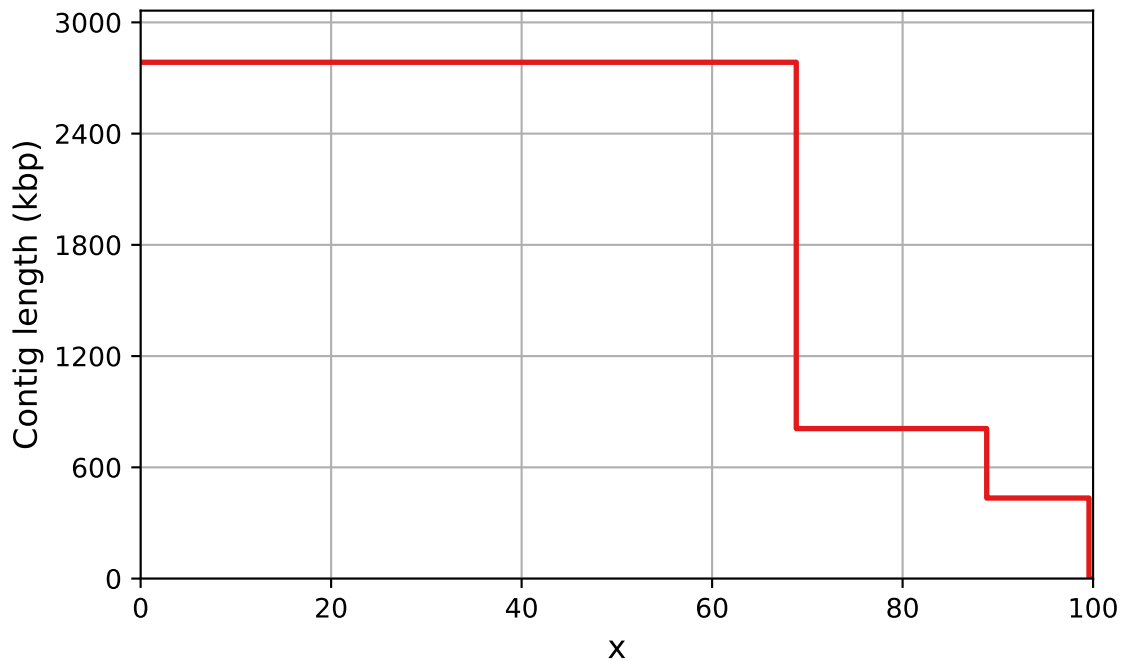


NAx



assembly

# NGAx



— assembly